AMENDMENTS TO THE CLAIMS

The following is a copy of Applicant's claims that identifies language being added with underlining ("___") and language being deleted with strikethrough ("—"), as is applicable:

1. (Withdrawn) A system for assaying multiple nucleic acid molecules in one or more biological samples having one or more nucleic acid targets per sample comprising:

a plurality of nucleic acid probes, wherein each nucleic acid of the plurality is different from other nucleic acids in the plurality, and

a plurality of intermediary nucleic acids, wherein each intermediary nucleic acid comprises a first region and a second region, wherein each intermediary nucleic acid is different from other intermediary nucleic acids in the plurality of intermediary nucleic acids by comprising a different first region, wherein the first region of each intermediary nucleic acid is complementary to a different nucleic acid probe of the plurality of nucleic acid probes, and wherein the second region of each intermediary nucleic acid is complementary to a potential target nucleic acid in a sample, wherein each probe of the plurality of nucleic acid probes and each second region of each intermediary nucleic acid comprises unstructured nucleotides, such that the second region of each intermediary nucleic acid has a reduced ability to form a stable duplex with a nucleic acid probe having regions of complementarity, wherein the second region of each intermediary nucleic acid forms a stable duplex with a complementary target nucleic acid, and wherein each nucleic acid probe forms a stable duplex with a complementary first region of an intermediary nucleic acid.

2. (Withdrawn) The system of claim 1, wherein the nucleic acid probes comprising modified and unmodified nucleotides and the second region of intermediary nucleic acids comprising modified nucleotides comprise complementary nucleotides that have a reduced ability to form base pairs with each other, wherein the modified nucleotides form base pairs with unmodified nucleotides.

3. (Withdrawn) The system of claim 1, wherein the modified nucleotides comprise A' and T' wherein A' and T' have a reduced ability to form a base pair, wherein A' forms a base pair with T*, and wherein T' forms a base pair with A*.

4. (Withdrawn) The system of claim 3, wherein A' is 2-aminoadenosine, wherein T is 2-thiothymidine, wherein A* is adenosine and wherein T* is thymidine.

5. (Withdrawn) The system of claim 1, wherein the modified nucleotides comprise G' and C' wherein G' and C' have a reduced ability to form a base pair, wherein G' forms a base pair with C*, and wherein C' forms a base pair with G*.

6. (Withdrawn) The system of claim 3, wherein G' is inosine, wherein C' is pyrrolopyrimidine, wherein G* is guanosine and wherein C* is cytosine.

7. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe corresponds to a known location in the array pattern.

8. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe associated with a known bead particle.

9. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe is associated with a defined tag moiety wherein the tag is detectable by mass electrophoretic mobility or optical property.

10. (Previously Presented) A method of assaying target nucleic acid molecules by tagging and sorting the target molecules with a universal array, comprising the steps of:

a) providing a first plurality of nucleic acids, wherein the first plurality of nucleic acids is immobilized on a surface such that different sequences of the first plurality of nucleic acids can be differentiated by location, wherein the nucleic acid at each location has a different nucleotide sequence than nucleic acids at other locations;

b) providing a second plurality of nucleic acids, wherein the nucleotide sequence of each nucleic acid of the second plurality is known and comprises a first region and a second region, wherein each first region of each nucleic acid of the second plurality has a different nucleotide sequence from other first regions of other nucleic acids of the second plurality, wherein each first region of nucleic acids of the second plurality is complementary to a nucleotide sequence of nucleic acids of the first plurality, wherein at least one second region of the nucleic acids in the second plurality is complementary to a target nucleic acid in a biological target, wherein each nucleic acid of the first plurality and each second region of each nucleic acid of the second plurality comprises unstructured nucleotides such that the second region has a reduced ability to hybridize to a first nucleic acid of the first plurality having a complementary nucleotide sequence without reducing the ability of the second region of each nucleic acid of the second plurality to hybridize to a complementary nucleic acid molecule in a biological target;

c) providing a biological target containing nucleic acids to be analyzed;

d) contacting the biological target with the second plurality of nucleic acids under conditions that permit hybridization of complementary nucleotide sequences between the target nucleic acid molecules and the second region of nucleic acids of the second plurality;

e) contacting the second plurality of nucleic acids with the first plurality of nucleic acids under hybridization conditions;

f) detecting nucleic acids in the biological target that have hybridized to a nucleic acid of the second plurality by detecting a signal of a label that is part of the nucleic acids of the biological target;

g) determining a location of the detectable signal of the label on the surface; and

h) determining the nucleotide sequence of the nucleic acid in the biological target that has hybridized to a nucleic acid of the second plurality by correlating the location of the signal to the nucleotide sequence.

11. (Original) The method of claim 10, wherein the steps of (d) and (e) are performed simultaneously.

12. (Original) The method of claim 10, wherein after step (e), unhybridized nucleic acids are removed.

13. (Previously Presented) The method of claim 10, wherein the step of detecting the label further comprises detecting the label by measuring light emission from the label.

14. (Previously Presented) The method of claim 10, wherein the step of contacting the biological sample with the second plurality of nucleic acids further comprises labeling the nucleic acids that having hybridized with a nucleic acid in the sample with a detectable label.

15.-18. (Canceled)

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a plurality of intermediary nucleic acids, wherein each intermediary nucleic acid comprises a first region and a second region, wherein each intermediary nucleic acid is different from other intermediary nucleic acids in the plurality of intermediary nucleic acids by comprising a different first region, wherein the first region of each intermediary nucleic acid is complementary to a different nucleic acid probe of the plurality of nucleic acid probes, and wherein the second region of each intermediary nucleic acid is complementary to a potential target nucleic acid in a sample, wherein each probe of the plurality of nucleic acid probes and each second region of each intermediary nucleic acid comprises unstructured nucleotides, such that the second region of each intermediary nucleic acid has a reduced ability to form a stable duplex with a nucleic acid probe having regions of complementarity, wherein the second region of each intermediary nucleic acid forms a stable duplex with a complementary target nucleic acid, and wherein each nucleic acid probe forms a stable duplex with a complementary first region of an intermediary nucleic acid.

2. (Withdrawn) The system of claim 1, wherein the nucleic acid probes comprising modified and unmodified nucleotides and the second region of intermediary nucleic acids comprising modified nucleotides comprise complementary nucleotides that have a reduced ability to form base pairs with each other, wherein the modified nucleotides form base pairs with unmodified nucleotides.

3. (Withdrawn) The system of claim 1, wherein the modified nucleotides comprise A' and T' wherein A' and T' have a reduced ability to form a base pair, wherein A' forms a base pair with T*, and wherein T' forms a base pair with A*.

4. (Withdrawn) The system of claim 3, wherein A' is 2-aminoadenosine, wherein T is 2-thiothymidine, wherein A* is adenosine and wherein T* is thymidine.

5. (Withdrawn) The system of claim 1, wherein the modified nucleotides comprise G' and C' wherein G' and C' have a reduced ability to form a base pair, wherein G' forms a base pair with C*, and wherein C' forms a base pair with G*.

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7. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe corresponds to a known location in the array pattern.

8. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe associated with a known bead particle.

9. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe is associated with a defined tag moiety wherein the tag is detectable by mass electrophoretic mobility or optical property.

10. (Previously Presented) A method of assaying target nucleic acid molecules by tagging and sorting the target molecules with a universal array, comprising the steps of:

a) providing a first plurality of nucleic acids, wherein the first plurality of nucleic acids is immobilized on a surface such that different sequences of the first plurality of nucleic acids can be differentiated by location, wherein the nucleic acid at each location has a different nucleotide sequence than nucleic acids at other locations;

b) providing a second plurality of nucleic acids, wherein the nucleotide sequence of each nucleic acid of the second plurality is known and comprises a first region and a second region, wherein each first region of each nucleic acid of the second plurality has a different nucleotide sequence from other first regions of other nucleic acids of the second plurality, wherein each first region of nucleic acids of the second plurality is complementary to a nucleotide sequence of nucleic acids of the first plurality, wherein at least one second region of the nucleic acids in the second plurality is complementary to a target nucleic acid in a biological target, wherein each nucleic acid of the first plurality and each second region of each nucleic acid of the second plurality comprises unstructured nucleotides such that the second region has a reduced ability to hybridize to a first nucleic acid of the first plurality having a complementary nucleotide sequence without reducing the ability of the second region of each nucleic acid of the second plurality to hybridize to a complementary nucleic acid molecule in a biological target;

c) providing a biological target containing nucleic acids to be analyzed;

d) contacting the biological target with the second plurality of nucleic acids under conditions that permit hybridization of complementary nucleotide sequences between the target nucleic acid molecules and the second region of nucleic acids of the second plurality;

e) contacting the second plurality of nucleic acids with the first plurality of nucleic acids under hybridization conditions;

f) detecting nucleic acids in the biological target that have hybridized to a nucleic acid of the second plurality by detecting a signal of a label that is part of the nucleic acids of the biological target;

g) determining a location of the detectable signal of the label on the surface; and

h) determining the nucleotide sequence of the nucleic acid in the biological target that has hybridized to a nucleic acid of the second plurality by correlating the location of the signal to the nucleotide sequence.

11. (Original) The method of claim 10, wherein the steps of (d) and (e) are performed simultaneously.

12. (Original) The method of claim 10, wherein after step (e), unhybridized nucleic acids are removed.

13. (Previously Presented) The method of claim 10, wherein the step of detecting the label further comprises detecting the label by measuring light emission from the label.

14. (Previously Presented) The method of claim 10, wherein the step of contacting the biological sample with the second plurality of nucleic acids further comprises labeling the nucleic acids that having hybridized with a nucleic acid in the sample with a detectable label.

15.-18. (Canceled)